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#2

OIPE

RAW SEQUENCE LISTING   DATE: 12/07/2001
PATENT APPLICATION: US/09/894,657   TIME: 12:56:28

Input Set : N:\Crf3\RULE60\09894657.txt
Output Set: N:\CRF3\12072001\I894657.raw

SEQUENCE LISTING
```
C--> 3  (1) GENERAL INFORMATION:
     5      (i) APPLICANT: Hillman, Jennifer L.
     6                     Yue, Henry
     7                     Lal, Preeti
     8                     Shah, Purvi
     9                     Corley, Neil C.
C-->11     (ii) TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
    12                              PROLIFERATION
    14    (iii) NUMBER OF SEQUENCES: 9
    16     (iv) CORRESPONDENCE ADDRESS:
    17          (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
    18          (B) STREET: 3174 Porter Dr.
    19          (C) CITY: Palo Alto
    20          (D) STATE: CA
    21          (E) COUNTRY: USA
    22          (F) ZIP: 94304
    24      (v) COMPUTER READABLE FORM:
    25          (A) MEDIUM TYPE: Diskette
    26          (B) COMPUTER: IBM Compatible
    27          (C) OPERATING SYSTEM: DOS
    28          (D) SOFTWARE: FastSEQ for Windows Version 2.0
    30     (vi) CURRENT APPLICATION DATA:
C-->31          (A) APPLICATION NUMBER: US/09/894,657
C-->32          (B) FILING DATE: 28-Jun-2001
    34    (vii) PRIOR APPLICATION DATA:
    35          (A) APPLICATION NUMBER: 09/410,372
    36          (B) FILING DATE:
    39   (viii) ATTORNEY/AGENT INFORMATION:
    40          (A) NAME: Billings, Lucy J.
    41          (B) REGISTRATION NUMBER: 36,749
    42          (C) REFERENCE/DOCKET NUMBER: PF-0421 US
    44     (ix) TELECOMMUNICATION INFORMATION:
    45          (A) TELEPHONE: 650-855-0555
    46          (B) TELEFAX: 650-845-4166
    49 (2) INFORMATION FOR SEQ ID NO: 1:
    51      (i) SEQUENCE CHARACTERISTICS:
    52          (A) LENGTH: 168 amino acids
    53          (B) TYPE: amino acid
    54          (C) STRANDEDNESS: single
    55          (D) TOPOLOGY: linear
    57    (vii) IMMEDIATE SOURCE:
    58          (A) LIBRARY: SYNORAB01
    59          (B) CLONE: 358673
    61     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
    63  Met Phe Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser
    64  1               5                   10                  15
```

ENTERED

RAW SEQUENCE LISTING   DATE: 12/07/2001
PATENT APPLICATION: US/09/894,657   TIME: 12:56:28

Input Set : N:\Crf3\RULE60\09894657.txt
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```
65  Ser Ala Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser
66              20              25              30
67  Gly Ser Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala
68          35              40              45
69  Ser His Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala
70      50              55              60
71  Gly Ala Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr
72  65              70              75              80
73  Glu Asp Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg
74              85              90              95
75  Ser Arg Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg
76          100             105             110
77  Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly
78          115             120             125
79  Leu Pro Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser
80      130             135             140
81  Ser Ser Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly
82  145             150             155             160
83  Arg Gly Ser Ser Ala Pro Ser Gln
84              165
86  (2) INFORMATION FOR SEQ ID NO: 2:
88      (i) SEQUENCE CHARACTERISTICS:
89          (A) LENGTH: 1105 base pairs
90          (B) TYPE: nucleic acid
91          (C) STRANDEDNESS: single
92          (D) TOPOLOGY: linear
94     (vii) IMMEDIATE SOURCE:
95          (A) LIBRARY: 358673
96          (B) CLONE: SYNORAB01
98      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
100  CGACCGTCCG CGGGAGACTG AGGTCCTGAG CCGACAGCCT CAGCTCCCTG CCAGGCCAGA      60
101  CCCGGCAGAC AGATGAGGGC CCAGGAGGCC TGGCGGGCCT GGGGGCGCTA CGGTGGGAGA     120
102  GGAAGCCAGG GGTACCTGCC TCTGCCTTCC AGGGCCACCG TTGGCCCCAG CTGTGCCTTG     180
103  ACTACGTAAC ATCTTGTCCT CACAGCCCAG AGCATGTTCC AGATCCCAGA GTTTGAGCCG     240
104  AGTGAGCAGG AAGACTCCAG CTCTGCAGAG AGGGGCCTGG GCCCCAGCCC CGCAGGGGAC     300
105  GGGCCCTCAG GCTCCGGCAA GCATCATCGC CAGGCCCCAG GCCTCCTGTG GGACGCCAGT     360
106  CACCAGCAGG AGCAGCCAAC CAGCAGCAGC CATCATGGAG GCGCTGGGGC TGTGGAGATC     420
107  CGGAGTCGCC ACAGCTCCTA CCCCGCGGGG ACGGAGGACG ACGAAGGGAT GGGGGAGGAG     480
108  CCCAGCCCCT TTCGGGGCCG CTCGCGCTCG GCGCCCCCCA ACCTCTGGGC AGCACAGCGC     540
109  TATGGCCGCG AGCTCCGGAG GATGAGTGAC GAGTTTGTGG ACTCCTTTAA GAAGGGACTT     600
110  CCTCGCCCGA AGAGCGCGGG CACAGCAACG CAGATGCGGC AAAGCTCCAG CTGGACGCGA     660
111  GTCTTCCAGT CCTGGTGGGA TCGGAACTTG GGCAGGGGAA GCTCCGCCCC CTCCCAGTGA     720
112  CCTTCGCTCC ACATCCCGAA ACTCCACCCG TTCCCACTGC CCTGGGCAGC CATCTTGAAT     780
113  ATGGGCGGAA GTACTTCCCT CAGGCCTATG CAAAAAGAGG ATCCGTGCTG TCTCCTTTGG     840
114  AGGGAGGGCT GACCCAGATT CCCTTCCGGT GCGTGTGAAG CCACGGAAGG CTTGGTCCCA     900
115  TCGGAAGTTT TGGGTTTTCC GCCCACAGCC GCCGGAAGTG GCTCCGTGGC CCCGCCCTCA     960
116  GGCTCCGGGC TTTCCCCCAG GCGCCTGCGC TAAGTCGCGA GCCAGGTTTA ACCGTTGCGT    1020
117  CACCGGGACC CGAGCCCCCG CGATGCCCTG GGGGCCGTGC TCACTACCAA ATGTTAATAA    1080
118  AGCCCGCGTC TGTGCAAAAA AAAAA                                         1105
```

RAW SEQUENCE LISTING   DATE: 12/07/2001
PATENT APPLICATION: US/09/894,657   TIME: 12:56:28

Input Set : N:\Crf3\RULE60\09894657.txt
Output Set: N:\CRF3\12072001\I894657.raw

```
120  (2) INFORMATION FOR SEQ ID NO: 3:
122       (i) SEQUENCE CHARACTERISTICS:
123             (A) LENGTH: 440 amino acids
124             (B) TYPE: amino acid
125             (C) STRANDEDNESS: single
126             (D) TOPOLOGY: linear
128      (vii) IMMEDIATE SOURCE:
129             (A) LIBRARY: LATRTUT02
130             (B) CLONE: 1352286
132      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
134  Met Arg Val Val Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala
135  1               5               10              15
136  Glu Leu Arg Lys Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His
137          20              25              30
138  Gly Arg Ala Gly Gly Gly Arg Arg Gly Ser Asn Pro Val Lys Arg Tyr
139          35              40              45
140  Ala Pro Gly Leu Pro Cys Asp Val Tyr Thr Tyr Leu His Glu Lys Tyr
141      50              55              60
142  Leu Asp Cys Gln Glu Arg Lys Leu Val Tyr Val Leu Pro Gly Trp Pro
143  65              70              75              80
144  Gln Asp Leu Leu His Met Leu Leu Ala Arg Asn Lys Ile Arg Thr Leu
145              85              90              95
146  Lys Asn Asn Met Phe Ser Lys Phe Lys Lys Leu Lys Ser Leu Asp Leu
147              100             105             110
148  Gln Gln Asn Glu Ile Ser Lys Ile Glu Ser Glu Ala Phe Phe Gly Leu
149          115             120             125
150  Asn Lys Leu Thr Thr Leu Leu Leu Gln His Asn Gln Ile Lys Val Leu
151          130             135             140
152  Thr Glu Glu Val Phe Ile Tyr Thr Pro Leu Leu Ser Tyr Leu Arg Leu
153  145             150             155             160
154  Tyr Asp Asn Pro Trp His Cys Thr Cys Glu Ile Glu Thr Leu Ile Ser
155              165             170             175
156  Met Leu Gln Ile Pro Arg Asn Arg Asn Leu Gly Asn Tyr Ala Lys Cys
157              180             185             190
158  Glu Ser Pro Gln Glu Gln Lys Asn Lys Lys Leu Arg Gln Ile Lys Ser
159          195             200             205
160  Glu Gln Leu Cys Asn Glu Glu Lys Glu Gln Leu Asp Pro Lys Pro Gln
161          210             215             220
162  Val Ser Gly Arg Pro Pro Val Ile Lys Pro Glu Val Asp Ser Thr Phe
163  225             230             235             240
164  Cys His Asn Tyr Val Phe Pro Ile Gln Thr Leu Asp Cys Lys Arg Lys
165              245             250             255
166  Glu Leu Lys Lys Val Pro Asn Asn Ile Pro Pro Asp Ile Val Lys Leu
167          260             265             270
168  Asp Leu Ser Tyr Asn Lys Ile Asn Gln Leu Arg Pro Lys Glu Phe Glu
169          275             280             285
170  Asp Val His Glu Leu Lys Lys Leu Asn Leu Ser Ser Asn Gly Ile Glu
171          290             295             300
172  Phe Ile Asp Pro Ala Ala Phe Leu Gly Leu Thr His Leu Glu Glu Leu
```

RAW SEQUENCE LISTING   DATE: 12/07/2001
PATENT APPLICATION: US/09/894,657   TIME: 12:56:28

Input Set : N:\Crf3\RULE60\09894657.txt
Output Set: N:\CRF3\12072001\I894657.raw

```
173  305                    310                   315                    320
174  Asp Leu Ser Asn Asn Ser Leu Gln Asn Phe Asp Tyr Gly Val Leu Glu
175                  325                   330                    335
176  Asp Leu Tyr Phe Leu Lys Leu Leu Trp Leu Arg Asp Asn Pro Trp Arg
177              340                    345                    350
178  Cys Asp Tyr Asn Ile His Tyr Leu Tyr Tyr Trp Leu Lys His His Tyr
179              355                    360                    365
180  Asn Val His Phe Asn Gly Leu Glu Cys Lys Thr Pro Glu Glu Tyr Lys
181      370                    375                    380
182  Gly Trp Ser Val Gly Lys Tyr Ile Arg Ser Tyr Tyr Glu Glu Cys Pro
183  385                    390                    395                    400
184  Lys Asp Lys Leu Pro Ala Tyr Pro Glu Ser Phe Asp Gln Asp Thr Glu
185              405                    410                    415
186  Asp Asp Glu Trp Glu Lys Lys His Arg Asp His Thr Ala Lys Lys Gln
187              420                    425                    430
188  Ser Val Ile Ile Thr Ile Val Gly
189          435                    440
191  (2) INFORMATION FOR SEQ ID NO: 4:
193         (i) SEQUENCE CHARACTERISTICS:
194             (A) LENGTH: 2082 base pairs
195             (B) TYPE: nucleic acid
196             (C) STRANDEDNESS: single
197             (D) TOPOLOGY: linear
199        (vii) IMMEDIATE SOURCE:
200             (A) LIBRARY: LATRTUT02
201             (B) CLONE: 1352286
203        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
205  GAATGCAGCC CATTCTCTGG AGAACTTCCT CACACACCGC AGCAAAGAGA AGACTGAAAG    60
206  ACAAACCTGG GTGCAGCCAG AGAGGTCCAG ATAGATGAGC TTGTGGCATC CATTCCCCAA   120
207  GTTCAGCCTA GGGACTCCAC GTACCCCAGC TGGGTCTCAT TGTTCCAGAA CTGCATTAGT   180
208  TAAGATTACC CAGACTTGGA TTTCAAAGGA ATACTTTCAT TGTTCCGTCT GTAACACGAA   240
209  GTAATTGGGG CCAGCTGGAT GTCAGGATGC GTGTGGTTAC CATTGTAATC TTGCTCTGCT   300
210  TTTGCAAAGC GGCTGAGCTG CGCAAAGCAA GCCCAGGCAG TGTGAGAAGC CGAGTGAATC   360
211  ATGGCCGGGC GGGTGGAGGC CGGAGAGGCT CCAACCCGGT CAAACGCTAC GCACCAGGCC   420
212  TCCCGTGTGA CGTGTACACA TATCTCCATG AGAAATACTT AGATTGTCAA GAAAGAAAAT   480
213  TAGTTTATGT GCTGCCTGGT TGGCCTCAGG ATTTGCTGCA CATGCTGCTA GCAAGAAACA   540
214  AGATCCGCAC ATTGAAGAAC AACATGTTTT CCAAGTTTAA AAAGCTGAAA AGCCTGGATC   600
215  TGCAGCAGAA TGAGATCTCT AAAATTGAGA GTGAGGCGTT CTTTGGTTTA AACAAACTCA   660
216  CCACCCTCTT ACTGCAGCAC AACCAGATCA AGTCTTGAC GGAGGAAGTG TTCATTTACA   720
217  CACCTCTCTT GAGCTACCTG CGTCTTTATG ACAACCCCTG GCACTGTACT TGTGAGATAG   780
218  AAACGCTTAT TTCAATGTTG CAGATTCCCA GGAACCGGAA TTTGGGGAAC TACGCCAAGT   840
219  GTGAAAGTCC ACAAGAACAA AAAATAAAA AACTGCGGCA GATAAAATCT GAACAGTTGT   900
220  GTAATGAAGA AAAGGAACAA TTGGACCCGA AACCCCAAGT GTCAGGGAGA CCCCCAGTCA   960
221  TCAAGCCTGA GGTGGACTCA ACTTTTTGCC ACAATTATGT GTTTCCCATA CAAACACTGG  1020
222  ACTGCAAAAG GAAAGAGTTG AAAAAAGTGC CAAACAACAT CCCTCCAGAT ATTGTTAAAC  1080
223  TTGACTTGTC ATACAATAAA ATCAACCAAC TTCGACCCAA GGAATTTGAA GATGTTCATG  1140
224  AGCTGAAGAA ATTAAACCTC AGCAGCAATG GCATTGAATT CATCGATCCT GCCGCTTTTT  1200
225  TAGGGCTCAC ACATTTAGAA GAATTAGATT TATCAAACAA CAGTCTGCAA AACTTTGACT  1260
226  ATGGCGTATT AGAAGACTTG TATTTTTTGA AACTCTTGTG GCTCAGAGAT AACCCTTGGA  1320
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```
227  GATGTGACTA CAACATTCAC TACCTCTACT ACTGGTTAAA GCACCACTAC AATGTCCATT  1380
228  TTAATGGCCT GGAATGCAAA ACGCCTGAAG AATACAAAGG ATGGTCTGTG GGAAAATATA  1440
229  TTAGAAGTTA CTATGAAGAA TGCCCCAAAG ACAAGTTACC AGCATATCCT GAGTCATTTG  1500
230  ACCAAGACAC AGAAGATGAT GAATGGGAAA AAAAACATAG AGATCACACC GCAAAGAAGC  1560
231  AAAGCGTAAT AATTACTATA GTAGGATAAG GTAGAAATTG TTCTGATTGT AATTAGTTTT  1620
232  GTATTTTCTA TACTGGTGTT AGAAAACATA TGTTTACATT TGATTAACTG TGTTGCCTAT  1680
233  TTATGCAGGG TAATCCAGCT AAAGGAAGCT TTCTTTAATT ATAAGTATTA TTGTGACTAT  1740
234  TATAGTAATC AAGAGAATGC TATCATCCTG CTTGCCTGTC CATTTGTGGA ACAGCATCTG  1800
235  GTGATATGCA ATTCCACACT GGTAACCTGC AGCAGTTGGG TCCTAATGAT GGCATTAGAC  1860
236  TTTCATAATG TCCTGTATAA ATGTTTTTAC TGCTTTTAGA AAATAAAGAA AAAAAACTTG  1920
237  GTTCATGTTT ACATGCCTTT CGATAGCTGT TTGTGCATAC TTAAAGATGA TCAAAATGAT  1980
238  TTTATACAAA TGCTGTTATA ATAAAATGTC ATTCCCTACC CCTCTACTTT TTTTCAGTAA  2040
239  GTCATCTTAT ACATTAAATA AATTTCCATT TCTGAAAAAA AA                      2082
241  (2) INFORMATION FOR SEQ ID NO: 5:
243       (i) SEQUENCE CHARACTERISTICS:
244           (A) LENGTH: 469 amino acids
245           (B) TYPE: amino acid
246           (C) STRANDEDNESS: single
247           (D) TOPOLOGY: linear
249      (vii) IMMEDIATE SOURCE:
250           (A) LIBRARY: OVARTUT01
251           (B) CLONE: 815087
253      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
255  Met Asp Val Glu Asn Glu Gln Ile Leu Asn Val Asn Pro Ala Asp Pro
256  1               5                   10                  15
257  Asp Asn Leu Ser Asp Ser Leu Phe Ser Gly Asp Glu Glu Asn Ala Gly
258              20                  25                  30
259  Thr Glu Glu Val Lys Asn Glu Ile Asn Gly Asn Trp Ile Ser Ala Ser
260          35                  40                  45
261  Ser Ile Asn Glu Ala Arg Ile Asn Ala Lys Ala Lys Arg Arg Leu Arg
262      50                  55                  60
263  Lys Asn Ser Ser Arg Asp Ser Gly Arg Gly Asp Ser Val Ser Asp Ser
264  65                  70                  75                  80
265  Gly Ser Asp Ala Leu Arg Ser Gly Leu Thr Val Pro Thr Ser Pro Lys
266              85                  90                  95
267  Gly Arg Leu Leu Asp Arg Arg Ser Arg Ser Gly Lys Gly Arg Gly Leu
268              100                 105                 110
269  Pro Lys Lys Gly Gly Ala Gly Gly Lys Gly Val Trp Gly Thr Pro Gly
270          115                 120                 125
271  Gln Val Tyr Asp Val Glu Glu Val Asp Val Lys Asp Pro Asn Tyr Asp
272      130                 135                 140
273  Asp Asp Gln Glu Asn Cys Val Tyr Glu Thr Val Val Leu Pro Leu Asp
274  145                 150                 155                 160
275  Glu Arg Ala Phe Glu Lys Thr Leu Thr Pro Ile Ile Gln Glu Tyr Phe
276              165                 170                 175
277  Glu His Gly Asp Thr Asn Glu Val Ala Glu Met Leu Arg Asp Leu Asn
278              180                 185                 190
279  Leu Gly Glu Met Lys Ser Gly Val Pro Val Leu Ala Val Ser Leu Ala
280          195                 200                 205
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VERIFICATION SUMMARY   DATE: 12/07/2001
PATENT APPLICATION: **US/09/894,657**   TIME: 12:56:29

Input Set : **N:\Crf3\RULE60\09894657.txt**
Output Set: **N:\CRF3\12072001\I894657.raw**

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]